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SEQUENCE LISTING <110> EVANS, RONALD M. <120> Novel steroid-activated nuclear receptors and uses therefor <130> SALK2270-5 <140> 10/081,555 <141> 2002-02-20 <150> 09/458,366 RECEIVED <151> 1999-12-09 <160> 09/227,718 AUG 3 0 2002 <161> 1999-01-08 <170> 09/005,286 TECH CENTER 1600/2900 <171> 1998-01-09 <180> 43 <190> PatentIn Ver. 2.1 **COPY OF PAPERS** ORIGINALLY FILED <210> 1 <211> 2068 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (583)..(1884) <220> <221> modified base <222> (1263) <223> a, c, t, or g <400> 1 ggcacgagga gatctaggtt caaattaatg ttgcccctag tggtaaagga cagagaccct 60 cagactgatg aaatgcgctc agaattactt agacaaagcg gatatttgcc actctcttcc 120 ccttttcctg tgtttttgta gtgaagagac ctgaaagaaa aaagtaggga gaacataatg 180 agaacaaata eggtaatete tteatttget agtteaagtg etggaettgg gaettaggag 240 gggcaatgga gccgcttagt gcctacatct gacttggact gaaatatagg.tgagagacaa 300 gattgtctca tatccgggga aatcataacc tatgactagg acgggaagag gaagcactgc 360 ctttacttca gtgggaatct cggcctcagc ctgcaagcca agtgttcaca gtgagaaaag 420

caagagaata agctaatact cctgtcctga acaaggcagc ggctccttgg taaagctact 480

ccttgatcga tcctttgcac cggattgttc aaagtggacc ccaggggaga agtcggagca 540

aagaacttac caccaagcag tccaagaggc ccagaagcaa ac ctg gag gtg aga Leu Glu Val Arg

L

ccc Pro 5	aaa Lys	gaa Glu	agc Ser	tgg Trp	aac Asn 10	cat His	gct Ala	gac Asp	ttt Phe	gta Val 15	cac His	tgt Cys	gag Glu	gac Asp	aca Thr 20	642
					aag Lys											690
					cgt Arg											738
					tgt Cys											786
					cgg Arg											834
					acc Thr 90											882-
					ggc Gly											930
gcc Ala	gtg Val	gag Glu	gag Glu 120	agg Arg	cgg Arg	gcc Ala	ttg Leu	atc Ile 125	aag Lys	cgg Arg	aag Lys	aaa Lys	agt Ser 130	gaa Glu	cgg Arg	97 8
			_		ctg Leu			-				_				1026
					ctg Leu											1074
					aag Lys 170									_	_	1122
					gag Glu											1170
					gtc Val											1218
					gga Gly											1266
agc Ser	cga Arg	cag Gln	tgg Trp 230	Arg	aaa Lys	gag Glu	atc Ile	ttc Phe 235	Ser	ctg Leu	ctg Leu	ccc Pro	cac His 240	Met	gct Ala	1314

					atg Met 250											1362
					gac Asp											1410
aag Lys	Gly 999	gcc Ala	gct Ala 280	ttc Phe	gag Glu	ctg Leu	tgt Cys	caa Gln 285	ctg Leu	aga Arg	ttc Phe	aac Asn	aca Thr 290	gtg Val	ttc Phe	1458
					acc Thr			_			_					1506
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					ctg Leu 330											1602
					atc Ile											1650
					gtg Val									Ile		1698
ctg Leu	aag Lys	tcc Ser 375	tac Tyr	att Ile	gaa Glu	tgc Cys	aat Asn 380	cgg Arg	ccc Pro	cag Gln	cct Pro	gct Ala 385	cat His	agg Arg	ttc Phe	1746
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					cgg Arg 410											1842
_	_			_	cag Gln		_						-			1884
tga	gcggd	etg (cctt	gggt	ga ca	acctt	cgaç	g agg	gçago	ccag	acco	agag	gcc d	ctcts	gagccg	1944
gca	ctcc	gg (gccaa	agaca	ag at	ggad	cacto	g cca	aagag	gccg	acaa	atgco	cct g	gctgg	gcctgt	2004
ctc	cctag	ggg a	aatto	cctg	ct at	gaca	agct	g gct	agca	attc	ctca	aggaa	agg a	acato	gggtg	2064
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<220>

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Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala 35 40 45

Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe 50 55 60

Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg 65 70 75 80

Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala 85 90 95

Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile 100 105 110

Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys 115 120 125

Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr 130 135 140

Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys 145 150 155 160

Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly
165 170 175

Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Pro Leu Gln Ala Pro Ser 180 185 190

Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser 195 200 205

Leu Lys Val Ser Leu Gln Ala Ala Gly Gly Gly Trp Gln Cys Leu Glu 210 215 220

Leu Gln Xaa Pro Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu 225 230 235 240

Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser 245 250 255

Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln 260 265 270

Ile Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe 275 280 285

Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu 290 295 300

Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu 305 310 315

Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His 325 330 335

Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp 340 345 350

Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln 355 360 365

Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro 370 375 380

Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu 385 390 395 400

Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
405
410
415

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Gly Ser

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-2205

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with spacer of 5 nucleotides

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N

nucleotides

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repeat response element with spacer of 1 nucleotides 4400> 26 agcttaggtc agtgaccta 19 2210> 27 2211> 20 2212> DNA 2213> Artificial Sequence 2223> Description of Artificial Sequence: Inverted repeat response element with spacer of 2 nucleotides 4400> 27 agcttaggtc acgtgaccta 20 210> 28 2211> 21 2212> DNA 2213> Artificial Sequence 2220> 2223> Description of Artificial Sequence: Inverted repeat response element with spacer of 3 nucleotides 4400> 28 agcttaggtc acagtgacct a 210 2210> 29 2211> 22 2212> DNA 2213> Artificial Sequence 220> 2213> Description of Artificial Sequence: Inverted repeat response element with spacer of 3 nucleotides 4210> 29 2211> 22 2212> DNA 2213> Artificial Sequence 2220> 2223> Description of Artificial Sequence: Inverted repeat response element with spacer of 4 nucleotides	<220>	·		
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